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Sequence Listing



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Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Ferrara, Napoleon
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Fong, Sherman
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.

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Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagcttctg gtgcnttttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
ggccacatc aagaagttca ccttcgtctg catggctctg tcactcacgc 350
tctgtttcgt gatgttttg acaccaacg tgtctgngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tatcctgggt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150
gttttgagca ccaaagtgt ttgagaaaat tttgatagac atnatcggag 200
tggantttgc ctttgagaa ntttgngntg ttcctttgcg gattttctcc 250
tttttcccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggctctac cctacctggg ggtgcacggt 400
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccgat tccgggtcacg gggagggcgc atntcaccgg gtggctgang 50
acactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100
cgtcctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattcttcc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcacacctg gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200
 tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
 ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
 tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350
 gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400
 gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
 ttaagtctct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500
 gacggctcct tcaccaacat ctggttctac ttcggcgctg tgggctcctt 550
 cctcttcata ctcattccagc tgggtgctgt catcgacttt gcgcactcct 600
 ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650
 tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgcgatcgc 700
 ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
 agggcaaggc cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800
 atcgctgctg tcctgccccaa ggtccaggac gccagccca actcgggtct 850
 gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900
 ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950
 ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000
 gtgggatgcc ccgagcattg tgggcctcat catcttcttc ctgtgcaccc 1050
 tcttcatcag tctgcgctcc tcagaccacc ggcaggtgaa cagcctgatg 1100
 cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150
 gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
 tcacctacag ctactccttc ttccatttct gcctggtgct ggctcactg 1250
 cacgtcatga tgacgctcac caactggtac aagcccgggtg agaccggaa 1300
 gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
 cagggtgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400
 aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450
 tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
 caccaatcag ccaggtgag cccccacccc tgcccagct ccaggacctg 1550
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caggctcctg cagagcccca tcccccgcc acaccacac ggtggagctg 1650
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 agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc ccccagggga ccctgcccc ttcttggaact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met	Gly	Ala	Cys	Leu	Gly	Ala	Cys	Ser	Leu	Leu	Ser	Cys	Ala	Ser	1	5	10	15
Cys	Leu	Cys	Gly	Ser	Ala	Pro	Cys	Ile	Leu	Cys	Ser	Cys	Cys	Pro	20	25	30	
Ala	Ser	Arg	Asn	Ser	Thr	Val	Ser	Arg	Leu	Ile	Phe	Thr	Phe	Phe	35	40	45	
Leu	Phe	Leu	Gly	Val	Leu	Val	Ser	Ile	Ile	Met	Leu	Ser	Pro	Gly	50	55	60	
Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75	
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90	
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105	
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120	
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135	
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150	
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165	
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180	

Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu		185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr		200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe		215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe		230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala		245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu		260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser		275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro		290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr		305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile		320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His		335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met		350	355	360
Leu	Asp	Ala	Thr	Gln	Gln	Gln	Gln	Gln	Gln	Val	Ala	Ala	Cys	Glu		365	370	375
Gly	Arg	Ala	Phe	Asp	Asn	Glu	Gln	Asp	Gly	Val	Thr	Tyr	Ser	Tyr		380	385	390
Ser	Phe	Phe	His	Phe	Cys	Leu	Val	Leu	Ala	Ser	Leu	His	Val	Met		395	400	405
Met	Thr	Leu	Thr	Asn	Trp	Tyr	Lys	Pro	Gly	Glu	Thr	Arg	Lys	Met		410	415	420
Ile	Ser	Thr	Trp	Thr	Ala	Val	Trp	Val	Lys	Ile	Cys	Ala	Ser	Trp		425	430	435
Ala	Gly	Leu	Leu	Leu	Tyr	Leu	Trp	Thr	Leu	Val	Ala	Pro	Leu	Leu		440	445	450
Leu	Arg	Asn	Arg	Asp	Phe	Ser										455		

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcatccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttccac ttctgctgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcaccc acgg 24

<210> 25
<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

tggcacagat cttcacccac acgg 24

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27

<211> 1351

<212> DNA

<213> Homo sapiens

<400> 27

gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctgacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150
aggctgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccgga aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
cgaggcttca ttcgttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
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 tggtttgctc ttgtcttttt cttttctttt taactaagaa tggggctggt 1200
 gtactctcac ttacttatc cttaaattta aatacatact tatgtttgta 1250
 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
 t 1351

<210> 28
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
 1 5 10 15
 Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
 20 25 30
 Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
 35 40 45
 Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
 50 55 60
 Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
 65 70 75
 Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
 80 85 90
 Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
 95 100 105
 Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
 110 115 120
 Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
 125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 29
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 ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300
 ttcgttcattg gctggcgccg aacc 324

<210> 30
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50
accgcgggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggtctccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcattcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgcccgc cgcgcgcgcgc cgcgcgcactg cagccccagg ccccgcccc 50

ccaccacacgt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100

gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150

tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgcctt caacctgctt tacaccttg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300

tccgagtggc cggcgtggct attgcagtgg gcatcttctt gttcctgatt 350

gcttttagtggt gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400

tttttatatg attattctgt tacttgattt tattgttcag tttctgtat 450

cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500

gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaacc aaatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650

gaatatgctg gagaggTTTT gagatttgtt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagaccc cgcgcgcaat cctagtgcatt tcctttgatg agaaaacaag 800

gaagatttcc tttcgtatta tgatcttgtt cactttctgt aattttctgt 850

taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900

ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950

ttttctttcc gttgctgaaa aatatttgaa acttggtggtc tctgaagctc 1000

ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050

cctttcttag catttttacc tgcagaaaaa ctttgatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcactggtat aattatatgt 1150
 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaaatcaga aagtatgaga tcctggtatg ttaagggaaa tccaaattcc 1250
 caattttttt tggctttttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgactttttac 1400
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acattttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
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 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
				110					115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
				125					130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
				140					145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
				155					160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
				170					175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
				185					190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
				200										

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
 tgattggagc tgtaaaaaan tcttcaggtg ttgtnatttt tttatatgat 50
 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tgggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300
 gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350
 gatcctgggt gtttggtgta cctacagata caggaaccag 390

<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttggcnctt tttagggaaa gatgtgttgt 50
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ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttta 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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cttgttttagc ccctgaaacc aggagcaaca gggnnacagct tcctggaggt 100
tggttggaac caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200
tggctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
accacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggcccaaaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50
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gacgctgcag tgtgaggagc ctgtctgcac tgaggagagc agctgccaca 150
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400
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acccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600
tgcagaggtc agctgcccgc ctctcttct ccttctacaa ggatggaagg 650
atagtgcaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700
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tttgttagaa taatgtagt aggtgagtgt aaataaatt atataaagt 1250
agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
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ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
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 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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Leu	Gly	Val	Leu	Trp	Val	Ala	Gln	Met	Leu	Leu	Ala	Ala	Ser	Phe	20	25	30	
Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	35	40	45	
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	50	55	60	
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val	65	70	75	
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe	80	85	90	
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp	95	100	105	
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly	110	115	120	
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys	125	130	135	
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro	140	145	150	
Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195	

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 46
 tgggctgtgt cctcatgg 18

<210> 47
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 47
 tttccagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
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ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttgga aa ggggatgtga atcttcctg cacctatgac 250
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300
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gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
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<210> 52

<211> 321

<212> PRT

<213> Homo sapiens

<400> 52

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Asp	Thr	Tyr	Gly	Arg	Pro	Ile	Leu	Glu	Val	Pro	Glu	Ser	Val	Thr	20	25	30	
Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro	35	40	45	
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg	50	55	60	
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp	65	70	75	
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His	80	85	90	
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met	95	100	105	
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro	110	115	120	
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val	125	130	135	
Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly	140	145	150	
Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys	155	160	165	
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln	170	175	180	
Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr	Leu	Ser	Thr	185	190	195	

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe
				200					205					210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile
				215					220					225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
				230					235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser
				245					250					255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr
				260					265					270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe
				275					280					285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr
				290					295					300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His
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Val	Tyr	Glu	Ala	Ala	Arg									
				320										

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atcccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

<400> 58
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ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150
agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200
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<210> 59

<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30
Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45
Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60
Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75
Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90
Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105
Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120
Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135
Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
				140					145					150
Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165
Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro

	170		175		180
Pro Lys Ser Arg	Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu			
	185	190			195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala			
	200	205			210
Gly Asn Glu Ala	Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val			
	215	220			225
Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly			
	230	235			240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu			
	245	250			255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro			
	260	265			270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val			
	275	280			285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly			
	290	295			300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln			
	305	310			315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr			
	320	325			330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro			
	335	340			345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro			
	350	355			360
Ser Met Ile Pro	Ser Gln Ser Arg Ala	Phe Gln Thr Val			
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu		230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val	
				575					580					585	
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe	
				590					595					600	
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile	
				605					610					615	
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu	
				620					625					630	
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp	
				635					640					645	
Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu						
				650					655						

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

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<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcaagtctct gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

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<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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				20				25						30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35				40						45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

50										55					60				
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly					
				65					70					75					
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala					
				80					85					90					
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr					
				95					100					105					
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe					
				110					115					120					
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly					
				125					130					135					
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr					
				140					145					150					
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe					
				155					160					165					
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys					
				170					175					180					
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala					
				185					190					195					
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg					
				200					205					210					
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu					
				215					220					225					
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His					
				230					235					240					
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala					
				245					250					255					
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile					
				260					265					270					
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His					
				275					280					285					
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg					
				290					295					300					
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr					
				305					310					315					
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu					
				320					325					330					
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala					

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Thr Glu Asp Gly	Gly Asp Ala Ser Pro Val	Leu Asn His Ala Ala			
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Val Pro Leu Ile	Ser Asn Lys Ile Cys Asn	His Arg Asp Val Tyr			
	365	370		375	
Gly Gly Ile Ile	Ser Pro Ser Met Leu Cys	Ala Gly Tyr Leu Thr			
	380	385		390	
Gly Gly Val Asp	Ser Cys Gln Gly Asp Ser	Gly Gly Pro Leu Val			
	395	400		405	
Cys Gln Glu Arg	Arg Leu Trp Lys Leu Val	Gly Ala Thr Ser Phe			
	410	415		420	
Gly Ile Gly Cys	Ala Glu Val Asn Lys Pro	Gly Val Tyr Thr Arg			
	425	430		435	
Val Thr Ser Phe	Leu Asp Trp Ile His Glu	Gln Met Glu Arg Asp			
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Leu Lys Thr					

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 70
 tgacatcgcc cttatgaagc tggc 24

<210> 71
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 71
 tacacgtccc tgtggttgca gatc 24

<210> 72
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 72

cggttcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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 agcctaactc catcccccggt ggccattact gcataaaata gagtgcattt 3300
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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	20	25	30	
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly	Ser	Thr	Asp	Ser	Gly	Pro	Ile	Arg	Gln	Ala	Glu	Ala	Arg	Gln
				695					700					705
Glu	Ala	Ala	Glu	Ser	Asn	Arg	Glu	Arg	Gly	Gln	Gly	Gln	Glu	Pro
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Val	Gly	Ser	Gln	Glu	His	Ala	Ser	Thr	Ala	Ser	Leu	Thr	Leu	Ile
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<210> 75
 <211> 483
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473
 <223> unknown base

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 ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100

 ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

 ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200

 gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

 aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

 agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350

 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

 tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

 gagaccctgc caccattcc atntccatcc aag 483

<210> 76
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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 76
 gtctcagcac gtgttctggt ctcagg 27

<210> 77
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<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
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<400> 78
tacctgcacg atgggcac 18

<210> 79
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<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 83
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

<400> 84
catcctgcaa catggtgaaa ccacgcctgg ctaattttgt tgtatTTTTg 50
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atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200
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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
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 20 25 30
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaaggga agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20						25				30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35					40					45

Ala Asp Gly Pro	Pro Ala Ala Asp Gly	Glu Asp Gly Gln Asp Pro	50	55	60
His Ser Lys His	Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile		65	70	75
Gln Ser Ala Ala	His Phe Val Met Phe Phe Ala Pro Trp Cys Gly		80	85	90
His Cys Gln Arg	Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys		95	100	105
Tyr Asn Ser Met	Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp		110	115	120
Cys Thr Ala His	Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly		125	130	135
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys		140	145	150
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu		155	160	165
Gln Thr Leu Asn	Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu		170	175	180
Pro Pro Ser Ala	Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser		185	190	195
Ala Ser Asn Phe	Glu Leu His Val Ala Gln Gly Asp His Phe Ile		200	205	210
Lys Phe Phe Ala	Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro		215	220	225
Thr Trp Glu Gln	Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val		230	235	240
Lys Ile Gly Lys	Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser		245	250	255
Gly Asn Gln Val	Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp		260	265	270
Gly Lys Lys Val	Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser		275	280	285
Leu Arg Glu Tyr	Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly		290	295	300
Ala Thr Glu Thr	Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala		305	310	315
Glu Pro Glu Ala	Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn		320	325	330

Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
				335					340					345	
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
				410					415					420	
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
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<220>
 <223> Synthetic oligonucleotide probe

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<210> 92
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<220>
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<400> 92
 ccaagccaac acactctaca g 21

<210> 93
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<220>
 <223> Synthetic oligonucleotide probe

<400> 93
 aagtggtcgc cttgtgcaac gtgc 24

<210> 94
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<400> 94
ggtcaaaggg gatatatcgc cac 23

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gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
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 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200		205		210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn					
	215		220		225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser					
	230		235		240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly					
	245		250		255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys					
	260		265		270
Glu Phe Ile Lys Lys Lys Lys					
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<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

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<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys	320	325	330
Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala		335	340	345
Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln		350	355	360
Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro		365	370	375
Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met		380	385	390
Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly		395	400	405
Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln		410	415	420
Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser		425	430	435
Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly		440	445	450
Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro		455	460	465
Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala		470	475	480
Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser		485	490	495
Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp		500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met		515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser		530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala		545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe		560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu		575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu		590	595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp		
	605	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His		
	620	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His		
	635	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu		
	650	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu		
	665	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn		
	680	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu		
	695	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr		
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Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile		
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 <223> Synthetic oligonucleotide probe

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<210> 104
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<220>
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 ggagaatgtg gccacaac 18

<210> 105
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<220>
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<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106

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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 106

atccacttca gcggacac 18

<210> 107

<211> 45

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 107

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<210> 108

<211> 2579

<212> DNA

<213> Homo sapiens

<400> 108

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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu
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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
				20					25					30

Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45

Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60

Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr
				80					85					90

Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe
				95					100					105

Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110					115					120

Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn
				125					130					135

Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr
				140					145					150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
				530					535					540
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
				545					550					555

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

aagcgtgaca gcgggcacgt c 21

<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

<400> 113

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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
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<210> 114

<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

Met	Ala	Pro	Arg	Gly	Cys	Ala	Gly	His	Pro	Pro	Pro	Pro	Ser	Pro	1	5	10	15
Gln	Ala	Cys	Val	Cys	Pro	Gly	Lys	Met	Leu	Ala	Met	Gly	Ala	Leu	20	25	30	
Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys
155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly
170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr
185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr
200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn
215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln
230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro
245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser
260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile
275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu
290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly
305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly
320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys
335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His
350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val
365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly
380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu
395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His
410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln
425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu	
				440					445					450	
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr	
				455					460					465	
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly	
				470					475					480	
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe	
				485					490					495	
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr	
				500					505					510	
Gly	Ile	Gln	Glu	Ser											
				515											

<210> 115
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 115
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<210> 116
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 116
 ctctctgagt gtacatctgt gtgg 24

<210> 117
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<220>
 <221> unsure
 <222> 33
 <223> unknown base

<400> 117
 gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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1

5

10

15

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggctg ctgggtgctgt gcgcgctgct cctgctcttg 50

gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

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gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
			20					25					30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35					40					45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50					55					60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val		65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly		80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr		95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr		110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile		125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser		140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn		155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser		170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser		185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln		200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile		215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro		230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala		245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe		260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys		275	280	285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaag 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50
ggcaggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
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 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300
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 tgttacaaaa taaaa 2365

<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	365	370	375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	380	385	390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	395	400	405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	410	415	420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	425	430	435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	440	445	450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	455	460	465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	470	475	480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	485	490	495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	500	505	510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	515	520	525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	530	535	540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	545	550	555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	560	565	570

Cys

<210> 133
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gtttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc cgggccccca ttcgggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtcac agagtcggcg cggcgcgga 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200

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ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agataccaaa cagctggtgc acagctttgc tgagggccag 400

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atTTTgGGGa aaataaatgt cTTtgtaaaa aaaaaaaaaa aaaaaaaaa 1998

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<210> 137
<211> 316
<212> PRT
<213> Homo sapiens
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<220>
<221> unsure
<222> 233
<223> unknown amino acid
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<400> 137
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          20          25          30
Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp
          35          40          45
Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu
          50          55          60
Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
          65          70          75
Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala
          80          85          90
Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
          95          100          105
Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe
          110          115          120
Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser
          125          130          135
Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
          140          145          150
Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys
          155          160          165
Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp
          170          175          180
Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
          185          190          195
Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val
          200          205          210
Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro
          215          220          225

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Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	230	235	240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	245	250	255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	260	265	270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	275	280	285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	290	295	300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	305	310	315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
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<400> 141
tgcgaaccag gcagctgtaa gtgc 24

<210> 142
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150
acttctttcc ttgcttcagc aacatgaggc ttttcttgtg gaacgcggtc 200
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agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300
aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350
ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcacacctg aggctctcaa aggttgggac cagggcttga 450
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 tgggtggctca tgccgtgtaat cccagcactt tggggggccaa ggagggtgga 2050
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 gcagctacta ttgaataaat acctatcctg gattttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20						25					30
Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35						40					45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50						55					60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65						70					75
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80						85					90
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
			95						100					105
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110						115					120
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125						130					135
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140						145					150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
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Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

ctttccttgc ttcagcaaca tgaggc 26

<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gccagagca ggaggatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

aataaagctt ccttaatgtt gtatatgtct ttgaagtaca tccgtgcatt 50

tttttttagc atccaacccat tcctcccttg tagttctcgc cccctcaa 100
caccctctcc cgtagccac ccgactaaca tctcagtctc tgaaaatgca 150
cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgccca ccaggacgga gcatggaggt cacagtacct 250
gccaccctca acgtcctcaa tggctctgac gcccgctgc cctgcacctt 300
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350
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tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45
Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu

110										115					120				
Asp	Glu	Gly	Ile	Tyr	Asn	Cys	Tyr	Ile	Met	Asn	Pro	Pro	Asp	Arg					
				125					130					135					
His	Arg	Gly	His	Gly	Lys	Ile	His	Leu	Gln	Val	Leu	Met	Glu	Glu					
				140					145					150					
Pro	Pro	Glu	Arg	Asp	Ser	Thr	Val	Ala	Val	Ile	Val	Gly	Ala	Ser					
				155					160					165					
Val	Gly	Gly	Phe	Leu	Ala	Val	Val	Ile	Leu	Val	Leu	Met	Val	Val					
				170					175					180					
Lys	Cys	Val	Arg	Arg	Lys	Lys	Glu	Gln	Lys	Leu	Ser	Thr	Asp	Asp					
				185					190					195					
Leu	Lys	Thr	Glu	Glu	Glu	Gly	Lys	Thr	Asp	Gly	Glu	Gly	Asn	Pro					
				200					205					210					
Asp	Asp	Gly	Ala	Lys															
				215															

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 tcttcccttg tagttctcgc cccctcaaat caccttctcc cttagcccac 100
 ccnactaaca tctcagtcctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcagc gggctcagtc tctttttctc tttggtgcca 200
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250
 aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300
 aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350
 ctctgaggag atgttccctc agttccgcat gaagatcatt aacctgaagc 400
 tggagcgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450
 gatgtgtcgg tgatgtgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200
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ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
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<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgcttgcct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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cgcggaacca gcgctcccg ccggacgtca cccccagtg gtgctggctcc 150
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<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro	
				20					25					30	
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly	
				35					40					45	
Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val	
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Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile	
				65					70					75	
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp	
				80					85					90	
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr	
				95					100					105	
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys	
				110					115					120	
Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly	
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Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr	
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Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg	
				155					160					165	
Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met	
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Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val	
				185					190					195	
Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg	
				200					205					210	
Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser	
				215					220					225	
Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu	
				230					235					240	
Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys	

	245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu	260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr	275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln	290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu	305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys	320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu	335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp	350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln	365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser	380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu	395	400	405
Lys Arg Val Leu Leu Gly Pro	410		

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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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atggagagcg gggcctacgg cgcggccaag gcgggaggct ccttcgacct 100
gcggcgcttc ctgacgcagc cgcagggtgt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tctgcattct atggtgaggg ctacagcaat 200
gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250
ctgccgctat ggcagtgcca tcgggggtgt ggccttcctg gcctcggcct 300
tcttcttggg ggtcgacgcg tatttcccc agatcagcaa cgccactgac 350
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cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450
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 gtgccccatg gctccagac tctgtctgtg ccgagtgtat tataaaatcg 1450
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 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe
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 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
 20 25 30
 Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly
 35 40 45
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val
 50 55 60
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly
 65 70 75
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala
 80 85 90
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val
 95 100 105
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe
 110 115 120
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro
 125 130 135
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr
 140 145 150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166
ccaggaggct catgggaaag tcc 23

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 168
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agggtgatca gtgagcagaa ggatgcccggt ggccgaggcc ccccaggtgg 100
ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250
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 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 169
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 Gly Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala
 20 25 30
 Cys Glu Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val
 35 40 45
 Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly
 50 55 60
 Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val
 65 70 75
 Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe
 80 85 90
 Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu

95										100					105				
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr					
				110					115					120					
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly					
				125					130					135					
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro					
				140					145					150					
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu					
				155					160					165					
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val					
				170					175					180					
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile					
				185					190					195					
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu					
				200					205					210					
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg					
				215					220					225					
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu					
				230					235					240					
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr					
				245					250					255					
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly					
				260					265					270					
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg					
				275					280					285					
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala					
				290					295					300					
Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val					
				305					310					315					
Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu					
				320					325					330					
Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro					
				335					340					345					
Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	His					
				350					355					360					
Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr	Gly	Leu	Ala	Leu	Trp	Phe	Asp					
				365					370					375					
Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln					

	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile		
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585
Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala	Asp		
	590		595		600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Gln Glu Asp Ser	Met		
	605		610		615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp	Gln		
	620		625		630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg	Leu		
	635		640		645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp	Val		
	650		655		660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala	Val		

665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly		
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly		
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro		
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg		
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln		
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg		
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg		
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser		
785	790	795
Trp Ile Gln Gln Val Val Thr		
800		

<210> 170
 <211> 1327
 <212> DNA
 <213> Homo sapiens

<400> 170
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 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200
 tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450
 ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcggatgag 500
 gagcactgtg actgtggcct ccaggggcccc tccagccgca ttgttggtgg 550

agctgtgtcc tccgaggggtg agtggccatg gcaggccagc ctccagggttc 600
 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650
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 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgctgg cctggagagg 750
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800
 agccatgact acgacgtggc gctgctgcag ctcgaccacc cgggtggtgcg 850
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 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgctgt 1050
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150
 ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
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 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

tgccctatgca ctgaggaggc agaag 25

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

aggcaggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50

ccaccgcccg ggctccgtgc cgccaagttt tcattttoca ctttctctgc 100

ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150

gctggaaaca ccaagaggtg gtttttgttt tttaaaactt ctgtttcttg 200

ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250

tctggagcct ctgctattgc tttgctgcg ggagccccgt accttttgg 300
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tgaggtcaaa ccatctgtga ggtttaacct cgcacctcc aaggacccag 400
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acacaagaga gaaagacgcc aatgtagttg tggttgactg gctccccctg 600
gccaccagc tttacacgga tgcggtcaat aataccaggg tgggtgggaca 650
cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700
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cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900
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gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100
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aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
350

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence .

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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cgagccacct cttcccctcc cccgcttccc tgtcgcgctc cgctggctgg 100
acgcgctgga ggagtggagc agcaccggc cggccctggg ggctgacagt 150
cggcaaagt tggcccgaag aggaagtggc ctcaaacc cggcaggtggc 200
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caccgcccct actccgggc tgcgcgcgc tcccgcgcc cagccctggc 400
atccagagta cgggtcgagc cggggccatg gagccccct ggggaggcgg 450
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ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550
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ggtctggaca ctccatcctt gccaaacctc taccctaaag tggccttaag 3050
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tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30	
Pro	Pro	Ala	Val	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45		
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60	
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75	
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90	
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105	
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120	
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135	
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150	
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165	
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180	
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr				

185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200					205					210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					

	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro	Ser
	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu	Asp
	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn	Leu
	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly	Gly
	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg	Arg
	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr	Asn
	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro	Ser
	575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala	Arg
	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro	Pro
	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro	Ala
	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu	Pro
	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg	Gly
	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser	Pro
	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp	Asp
	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala	Glu
	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		
	710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtcacca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgctgtctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
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 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
			20						25					30

Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
			35						40					45

Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
			50						55					60

Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
			65						70					75

Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
			80						85					90

Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
			95						100					105

Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
			110						115					120

Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
			125						130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 78, 212, 234, 487

<223> unknown base

<400> 191

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catgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250
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gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450
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<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 192

cgttttgcag aacctactca ggcag 25

<210> 193

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgctgagc cgcggtgcc ggacgggacg 50

ggacgggcta ggctggggcg gcccccggg ccccgccgtg ggcattggcg 100

cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150

gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200

cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggaccctg 250

ccgagcgcca cgccgacggc ttggcgctcg ccttggagcc tgccctggcg 300

tcccccgcg ggcccgccaa cttcttggcc atggtagaca acctgcaggg 350

ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400

agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450

ggaacccgc actcctacat agacacgtac ttgacacag agaggtctag 500

cacataccgc tccaagggtt ttgacgtcac agtgaagtac acacaaggaa 550

gctggacggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600

aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650

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cacttgccaa gccatcaagt tctctggaga ccttcttcga ctccctgggtg 750

acacaagcaa acatccccaa cgttttctcc atgcagatgt gtggagccgg 800

cttgcccggt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900

gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
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<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
			35						40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
			50						55					60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile	350	355	360
Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile	365	370	375
Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn	380	385	390
Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu	395	400	405
Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp	410	415	420
Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu	425	430	435
Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr	440	445	450
Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu	455	460	465
Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly	470	475	480
Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg	485	490	495
Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser	500	505	510
Ser Leu Val Arg His Arg Trp Lys	515		

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggtc gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

<400> 205
cgctccgcc ttcgagggt gacgcgccg ggcgcgttc caggcctgtg 50
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gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200
ccccgccgtg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300
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 ttccgggcgg atgcagggct ggggtcatct gtatctgaag cccctcgga 1900
 taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	
				80					85					90	
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	
				95					100					105	
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	
				110					115					120	
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	
				125					130					135	
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	
				140					145					150	
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	
				155					160					165	
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	
				170					175					180	
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	
				185					190					195	
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	
				200					205					210	
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	
				215					220					225	
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	
				230					235					240	
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	
				245					250					255	
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	
				260					265					270	
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	
				275					280					285	
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	
				290					295					300	
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	
				305					310					315	
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	
				320					325					330	
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	
				335					340					345	
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	
				350					355					360	

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttgacttg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

ggaggagaca gcctcctggg gggcaggggt tccctgcctc tgctgctcct 50

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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150

caagcctcag gccagccacc tcccaccatc cgctggttgc tgaatgggca 200

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<210> 211
 <211> 985
 <212> PRT
 <213> Homo sapiens

<400> 211
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 20 25 30
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
 35 40 45
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
 50 55 60
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
 65 70 75
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
 80 85 90
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
 95 100 105
 Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
 110 115 120
 Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
 125 130 135

Cys Gly Pro Pro	Trp Gly His Pro Glu	Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln	Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg	Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn	Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln	Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg	Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu	Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser	Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr	Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu	Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly	Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg	Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val	Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly	Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn	Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser	Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu	Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala	Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys	Leu Leu Leu Glu Gln Ala	410	415	420

Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr				425	430	435
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala				440	445	450
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val				455	460	465
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly				470	475	480
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met				485	490	495
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr				500	505	510
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg				515	520	525
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu				530	535	540
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp				545	550	555
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser				560	565	570
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu				575	580	585
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp				590	595	600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu				605	610	615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln				620	625	630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu				635	640	645
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser				650	655	660
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala				665	670	675
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg				680	685	690
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr				695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 212
gaagggacct acatgtgtgt ggcc 24

<210> 213
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
ctcccacggt gtccagcgcc cagaatgcgg cttctggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350
cgaaaaacgg ggccccgatg agtctttact gatctctctg ttcgtctttc 400
caggaccctg ctgtcctccc tccccctctc ccacctteca gcctctggct 450
acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500
attgacttct cctgggtctt acccggcagc caccacagcc aagcagggga 550
agacaggggc tgaggcccct ccattgccag ggacttcca gtacgggcac 600
gaaaggactt ctcagtacac aggaacctt cctcaccag cgacctctcc 650
tcctgcaggg agtcccgcc ccccatgca gctggactcc acctcagcag 700
aggacaccag tccagctctc agcagtggca gctctaagcc caggggtgtcc 750
atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800
gtcagccgca ggctgatcg cttctgcag ccacctgctc ctgtggagaa 850
aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900
tcacgcttga ctgcgaggga aaaggaagcc ccttcccagg cccctgaggg 950
ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctgggct 1000
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cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100
cacctcagcc tcagagtcca gctgcccgga ctccagggt ctccccacc 1150
tccccaggct ctctcttgc atgttcacgc ctgacctaga agcgtttgtc 1200
agccctggag ccagagcgg tggccttgct cttccggctg gagactggga 1250
catccctgat aggttcacat ccctgggcag agtaccaggc tgctgaccct 1300
cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350
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ccagaccca ccttgtcttc cctccctggc gtctcagac ttagtccac 1450
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ggattctggc ttctctttga accacctgca tccagccctt caggaagcct 1550
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tgtctgcgac accagatcca cgtggggact cccctgaggc ctgctaagtc 1800
 caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850
 acagaagtgg ttgcctttnc catttgcctt ccttggacca tgccttcttg 1900
 cctttggaaa aaatgatgaa gaaaaccttg gctccttcct tgtctggaaa 1950
 ggggttacttg cctatgggtt ctgggtggcta gagagaaaag tagaaaacca 2000
 gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050
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 gtaaagtagc acaactacta ttttttttct ttttccatta ttattgtttt 2150
 ttaagacaga atctcgtgct gctgcccagg ctggagtgca gtggcacgat 2200
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 cttttagtag agatgggggtt tcaccatggt ggccaggctg gtcttgaact 2350
 cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gccgggatta 2400
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 agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500
 gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550
 tttgtgttac ttcttccac tcttttcttc ttacataat ttgccggtgt 2600
 tctttttaca gagcaattat cttgtatata caactttgta tctgccttt 2650
 tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700
 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
1				5					10					15

Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20					25					30

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40					45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

[illegible]

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggt gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggtgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
ggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150
tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctcttctgt gaggggacga cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
ccgccggcat agaagccagg agcagggctc tcagaaggcg gtggtgacca 400

gctgggatca tgttgttggc cctgggtctgt ctgctcagct gcctgctacc 450
 ctccagttag gccaaagtct acggtcggtt tgaactggcc agagtgtac 500
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser	1	5	10	15
Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu	20	25	30	
His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp	35	40	45	
Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala	50	55	60	
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln	65	70	75	
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro	80	85	90	
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu	95	100	105	
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln	110	115	120	
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys	125	130	135	
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe	140	145						

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tgttggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggccggg cgcccgggc gccaccatga gtccccgctc 50
gtgcctgcgt tcgctgcgcc tctcgtctt cgccgtcttc tcagccgccg 100
cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200
gatgtgcaag cggaacctgg aagtcattga ctccgtgcgc cgcgggtgcc 250
agctggccat tgaggagtgc cagtcaccgt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctc ggcaagggtg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
ctctgacaac atcgcttacg gtgtggcctt ctcacagtgc tttgtggatg 550
tgccggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc cacgggggtg caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgagggtga gccacgccgc gtgggtcctt ccagggcact 800
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900
ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050
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aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200
ctggtttggt ttttgggtcc tcatgttatt tattgccga accaggcagg 1250
caacccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
ctgccactga ccaaagggac cttgctcgtg ccgctggctg cccgcatgtg 1350
gctgccactg accactcagt tgttatctgt gtccgttttt ctacttgag 1400
acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450
gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500
atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550
tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaag 1600
ccctgagaaa ggaacaagc agataccagg tcaagggcac caggttcatt 1650
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cccagcctgc cccagcctgc ccctgggaag aggaactta accactcccc 1800
agaccacct aggcaggcat ataggctgcc atcctggacc agggatcccc 1850

gctgtgcctt tgcagtcacg ccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000
ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	1	5	10	15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	20	25	30	
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	35	40	45	
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	50	55	60	
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	65	70	75	
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	80	85	90	
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	95	100	105	
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	110	115	120	
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135	
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150	
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165	
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180	
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195	
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210	
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro				

215										220					225				
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly					
				230					235					240					
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu					
				245					250					255					
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu					
				260					265					270					
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg					
				275					280					285					
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser					
				290					295					300					
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe					
				305					310					315					
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe					
				320					325					330					
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val					
				335					340					345					
Glu	Leu	His	Thr	Cys	Arg														
				350															

<210> 227
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 227
 gctgcagctg caaattccac tgg 23

<210> 228
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 228
 tgggtgggaga ctgtttaaat tatcggcc 28

<210> 229
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500
caactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550
gcgagccgtg cccacgctc tggctgtcct tcgagggctc ctgctacttt 600
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700
tcaactcgaa cagcgtggc cgtggttact ggctgggcct gagggtgtg 750
cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800
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agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg taccctgggg 1000
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tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100
tgtccagccc agtgccctggg ctctggggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
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 gtgactgagg actggagctg ttgggttttc tcgcattttc caccaaactg 1300
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<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp
275 280 285

Ile Cys Glu Lys Arg His Asn Cys
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

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ctccacgctc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200
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 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

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				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val
				110					115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165

Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala	
	170	175	180
Ala Leu Asp Leu Tyr	Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe		
	185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr Ile	Pro Gln Asp Thr Val	
	200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser His	Pro Ala Asn Ser Phe	
	215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr	
	230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala	
	245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu Ile	Val Asp Ser Ala Ser	
	260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser	
	275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly Arg	Leu Gly Thr Lys Ser	
	290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro	
	305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys	
	320	325	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccttc tctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagccccttc tctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244
ggcggcgctcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300
cagaaatttt atccaacttt gtttgaagc ttattatgac aataccattt 350
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 catgtgtttt ttctagctg accttttata ttgctaaatc tgaaataaaa 1850
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 245
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
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 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
 20 25 30
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
 35 40 45
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
 50 55 60
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
 65 70 75
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
 80 85 90
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
 95 100 105
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
 110 115 120
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
 125 130 135

Asp Thr Val Tyr	Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tggtgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
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<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
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 aaaaaa 2456

<210> 254

<211> 545

<212> PRT

<213> Homo sapiens

<400> 254

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Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly	35	40	45	
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser	50	55	60	
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly	65	70	75	
Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg	80	85	90	
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met	95	100	105	
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe	110	115	120	
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro	125	130	135	

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala	290	295	300
Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp	305	310	315
Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser	320	325	330
Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile	350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgcctgc aggagtcctg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacctcagg aagccgaaga tgcc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257

gaacggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50
actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100
ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150
tgcatctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200
gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250
aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300
acccggggcc gattccagct cactggggat cccgccaagg ggaactgctc 350
cttgggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400
gggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450
tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500
caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550
agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttgttatc 600
agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650
tgtcccatac ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700
ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750
gtcctctcct cgtcccatcc ctggggccct agaccctgg ggctggagct 800
gcccgggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850
acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900
ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtcttgga 950
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gcctggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050
cagaggggac aggttctgag cccctcccag ccctcagacc ccggggctct 1100
ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150
ctcggcacc actgggtccc cagcacgtct ctctcagcct ctccgtgcac 1200

tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
aatcggcatc acggctcttc ttttcctctg cctggccctg atcatcatga 1300
agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350
tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400
ccccctgggt cagaagcggg atcagaaaag cacaccaaag agtcctcgga 1450
cccctcctcc accaggtgct cctccccag aatcaaagaa gaaccagaaa 1500
aagcagtatc agttgccag tttcccagaa cccaaatcat cactcaagc 1550
cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600
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agtgc aaagt ttccttctct cctctctct ctctcttct ctctctctct 1800
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tcgggagttc gagaccagcc tggccaactt ggtgaaaccc cgtctctact 1950
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tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
tgcagtgagc caagatcaca ccattgcag ccagcctggg caacaaagcg 2100
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aaacatagct gggcttgggt gtgtgtgcct gtagtcccag ctgtcagaca 2300
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gagacctact gggctgcatt ctgagacagt ggaggcattc taagtcacag 2400
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aaaacagatt gcagtaaaga agccaaccaa atcccaccaa aaccaagttg 2500
gccacgagag tgacctctgg tcgtctcac tgctacactc ctgacagcac 2550
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<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259

Met	Leu	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	Leu	Gly	Gly	Ser	Gln	1	5	10	15
Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met	20	25	30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp	50	55	60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr	65	70	75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe	80	85	90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile	95	100	105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val	110	115	120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe	125	130	135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp	140	145	150	
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly	155	160	165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro	170	175	180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu	185	190	195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys	200	205	210	
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro	215	220	225	

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350
tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400
tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450
tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600
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 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
 atttaaa 2857

<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

Met	Asn	Cys	Tyr	Leu	Leu	Leu	Arg	Phe	Met	Leu	Gly	Ile	Pro	Leu		1	5	10	15
Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys		20	25		30
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp		35	40		45
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser		50	55		60
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70		75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85		90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100		105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115		120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130		135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145		150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160		165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175		180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190		195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205		210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220		225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235		240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250		255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265		270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280		285

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser	290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile	305	310	315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr	320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu	335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln	350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr	365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly	380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg	395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly	410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp	425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln	440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp	455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu	470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp	485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser	500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln	515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu	530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn	545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val	560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	
				575					580					585	
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	
				590					595					600	
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	
				605					610					615	
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	
				620					625					630	
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	
				635					640					645	
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
				650					655					660	
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
				665					670					675	
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
				740					745					750	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
				755					760					765	
Ser	Ala	Val	Gln	Ser	Asn	Asn									
				770											

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50

gaatatttttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100

attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagtat ccagactcca gcgccgcccc gggcgcgagc 50

cccaaccccg acccagagct tctccagcgg cggcgcgagc agcagggctc 100

cccgccttaa cttctccgc ggggcccgac caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250
cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300
cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350
gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400
gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450
aagcaaccgc tgccttgatg gtggttgga tctcctggg agtgatagca 500
atctttgtgg ccaccgttgg catgaagtgt atgaagtgt tggaagacga 550
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gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900
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gttaaaatac tcagtgttaa acatggctta atcttatttt atcttctttc 1050
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gtaatcatal tcaaatgggg gaaggggtgc tcttaaata tatatagata 1150
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cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
atttaattcc atattgatga agatgtttat tggatatatt tctttttcgt 1300
ccttatatac atatgtaaca gtcaaatatc atttactctt cttcattagc 1350
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tttcaattct tcatgcgtgc ctttttcata tacttatttt attttttacc 1450
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cttcatctgt aagcgggtgt ttgtaattcc tgatcttccc acctcacagt 2600
gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgттаag 2747

<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25										30									
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala															
				35					40					45															
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly															
				50					55					60															
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser															
				65					70					75															
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu															
				80					85					90															
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met															
				95					100					105															
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val															
				110					115					120															
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val															
				125					130					135															
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp															
				140					145					150															
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu															
				155					160					165															
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala															
				170					175					180															
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr															
				185					190					195															
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr															
				200					205					210															

Val

<210> 271

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 21, 69, 163, 434, 436, 444

<223> unknown base

<400> 271

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ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttgaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450
 gaccttatga cccagtc aa tgccaggtac gaatttggtc aggtctctct 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttcctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
 tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
 cntcagcact gccctgcccc agtggaggat ttactcctat nccggnaca 150
 acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgctgtg 200
 tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgtgtga 250
 atctgagcag cacattgcaa gcaaccctgt ccttgatggt ggttggcatc 300
 ctctggggag tgatagcaat cttnttggcc accgttgttn ntgaagtgt 350
 tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
 gggggcgcca tatttcttct tgcaggtctg gctatttttag ttgccacagc 450
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccctat 100
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtggttg 250
gcatectcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttggaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacagg tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcgttcaa gaattctatg accctatgac 450
cccagtcaat gccaggtacg aatttggtca ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctcccct cctggatgga tcgcnccacc gtcacattgc cttcccccan 50
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
ttaccgaggg gctttgatg tcntgcntgt cgcagagcac cgggcagatc 150
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccctgac cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400
cnngnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450

tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

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gcagcacatt ncaagcaacc ccttgcccttg aaggtggttg ncatcccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300

tgccaggtag gaatttggtc aggtctctct cactggctgg gctgctgctt 350

ctctctgcct tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

agcaatgccc tgccccaggt ggaggattaa ttcctatgnt ggggacaaca 50

ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcatcttcc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatatatt cttnttgcag gtctggctat tttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50

cacagcatgg tatggcaata gaatcggtca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttgggc aggctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttctctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacnccat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaacctg 200

ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgt tgaagtgtt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgca tatttcttct tgcaggtctg 350

gctatttttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtacgaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgcttctctc tgccttcttg gaggtgccct 500

actttgctgt tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
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acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtga aagtctttga ctcttgctg 200
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ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
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ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttgtgtt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

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ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100

tagaggaccc ccgcccgtgc cccgaccggt ccccgacctt ttgtaaaact 150

taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200

ctccccgcca aagggtgtcc gccgctaagg aacatggcga aggtggagca 250

ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

ccgatgttgt caccaccaac cttaaagcttg gcaacccgac agaccgaaat 350

gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400

caacagcggg atcatcgatg caggggcctc aattaatgta tctgtgatgt 450

tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500

gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550

gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600

ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650

attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700

tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750

gtaagaggct gcaagggtgaa gttcagaggc tacgggagga gaacaagcag 800

ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850

ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900

ggctcttggc tctggtgggt ttgttcttta tcgttggtgt aattattggg 950

aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattgggtg 1000

gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgaatgacatc tcacaggtct tgcctttaaa ttaccctcc 1100
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
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ctttattaat gacaagggaa accatgagta atgccacaat ggcatattgt 1250
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
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tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200
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agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255
<223> unknown base

<400> 285
gtcagtcttc tagattgtcc ttatcccacc tttcaaccan tactcacatt 50
tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 73, 97
<223> unknown base

<400> 286
tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50
gattacctcc ttaaatagaca ccnttctctg cctggttggtg ctggccnttg 100
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcttt 350
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287
<211> 270

<212> DNA
<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50
ctttagtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288

ggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttghta taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgtt tggtcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaattgca tatttaantt atttaattga tttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
atttaactta tttaatgtat ttcattctcat gttttcttat tgcacaaga 300
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
gaaacntgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
ggggagtgcg gtctgtccca cacagtagtc cccangtggc ccantcccg 250
cccaggctgc ttccgtgtc ttcagttctg tccaagccat cagctccttg 300
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgatttg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcataatt aanttattta atgtatttca tntcatgttt tcttattgtc 550
acaagggtac agttaatgct gcgtgctgct gaantctgtt gggatgaantg 600
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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cacagtagtc cccacgtggc ccaactcccgg cccaggctgc tttccgtgtc 100
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250
tgctttgttc acttaaagg accaagctaa atttgtattg gttcatgtag 300
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggctg 450
tgggctcctc tgtctctgga gagtctggc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50
ggctggctga gaggtccca gctgcagcgt ccccgccgc ctcccgga 100
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200
tgacgccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
acaggacaaa attagaagat caaatggaa aatatgctgc tttggttgat 300
atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350
attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450
tacagtgtgt ggcatcgaat gccagaaaga actcccaact cccagccttt 500
ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550
cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600
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gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750
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 aatgtgaaat tgcatagata aaggtagatg gttaaagcaat tagtatcaga 1950
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 ttcagctcat gccctcaatg tttatattgt gttatctggt gggctctggga 2050
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
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 caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200
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 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20										25					30				
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu					
				35					40					45					
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr					
				50					55					60					
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu					
				65					70					75					
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn					
				80					85					90					
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu					
				95					100					105					
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg					
				110					115					120					
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp					
				125					130					135					
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu					
				140					145					150					
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu					
				155					160					165					
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly					
				170					175					180					
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser					
				185					190					195					
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala					
				200					205					210					
Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu					
				215					220					225					
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln					
				230					235					240					
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys					
				245					250					255					
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp					
				260					265					270					
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala					
				275					280					285					
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys					
				290					295					300					
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp					

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu		
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser		
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys		
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp		
365	370	375
Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg		
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly		
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcgttccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggaggc cttcctttca gtggaccgg gtcaagaata ccac 45

<210> 300

<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300

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ccagtactgg atgtgacagc aggacagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
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cagaacatgc agtaatgtgg actgcccacc agaagcaggc gatttccgag 400
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tcacttatat ctggaaacca aaaccctcca ggggactaaa ggtgaaaaca 850
gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc 900
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 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
 taagtgtaat catctacca aagctttttg gctctcaaat taaagattga 1850
 ttagtttcaa aaaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggcc 50
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100
 ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
 cgccgaggag gcggcgggtc agctccgccg cgagctccgc caggccgcgg 350
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400
 gagctggacc tcgcctcgct gcgctcgggt cgcgccttct gccaggaaat 450
 gctccaggaa gaggcctaggc tggatgtctt gatcaataac gcagggatct 500
 tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
 gtgaaccatc tggggcactt totactcacc aatcttctcc ttggactcct 600
 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcaccgtc aatgtgttgc 800
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900
 agtagaaggt gccagactt ccatttattt ggcctcttca cctgaggtag 950
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050
 agtgatgggtt ggcctgctaa aataggaaca aggagtaaaa gagctgttta 1100
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtatttttg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5					10				15	

Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20						25				30	

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35					40				45	

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
				50					55				60	

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
				65					70				75	

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
				80					85				90	

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Val Gly Glu Leu	Ile Val Arg Glu Leu	Asp Leu Ala Ser Leu	Arg
	110	115	120
Ser Val Arg Ala	Phe Cys Gln Glu Met	Leu Gln Glu Glu	Pro Arg
	125	130	135
Leu Asp Val Leu	Ile Asn Asn Ala Gly	Ile Phe Gln Cys Pro	Tyr
	140	145	150
Met Lys Thr Glu	Asp Gly Phe Glu Met	Gln Phe Gly Val Asn	His
	155	160	165
Leu Gly His Phe	Leu Leu Thr Asn Leu	Leu Leu Gly Leu Leu	Lys
	170	175	180
Ser Ser Ala Pro	Ser Arg Ile Val Val	Val Ser Ser Lys Leu	Tyr
	185	190	195
Lys Tyr Gly Asp	Ile Asn Phe Asp Asp	Leu Asn Ser Glu Gln	Ser
	200	205	210
Tyr Asn Lys Ser	Phe Cys Tyr Ser Arg	Ser Lys Leu Ala Asn	Ile
	215	220	225
Leu Phe Thr Arg	Glu Leu Ala Arg Arg	Leu Glu Gly Thr Asn	Val
	230	235	240
Thr Val Asn Val	Leu His Pro Gly Ile	Val Arg Thr Asn Leu	Gly
	245	250	255
Arg His Ile His	Ile Pro Leu Leu Val	Lys Pro Leu Phe Asn	Leu
	260	265	270
Val Ser Trp Ala	Phe Phe Lys Thr Pro	Val Glu Gly Ala Gln	Thr
	275	280	285
Ser Ile Tyr Leu	Ala Ser Ser Pro Glu	Val Glu Gly Val Ser	Gly
	290	295	300
Arg Tyr Phe Gly	Asp Cys Lys Glu Glu	Glu Leu Leu Pro Lys	Ala
	305	310	315
Met Asp Glu Ser	Val Ala Arg Lys Leu	Trp Asp Ile Ser Glu	Val
	320	325	330
Met Val Gly Leu	Leu Lys		
	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229
<223> unknown base

<400> 304
ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaattat ctgcctggct t 521

<210> 305
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 305
ccaggaaatg ctccaggaag agcc 24

<210> 306
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 306
gcccatgaca ccaaattgaa gagtgg 26

<210> 307
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307

aacgcagga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttctatcc ttacccgacc tcagatgctc ctttctgctc ctggtaactt 200
gggttttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa attttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatattt gcatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttacia ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggc atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
 gcttttaaaaaa cttgaaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195	

Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 48

<223> unknown base

<400> 310

attaaggaag aattttccaaa tgaaaatcaa gtagtntttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgcnng agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagcgctctg tccctgtcnc ggancccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250
gggttttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gcttttagtca atttttatgc 350
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttccta tccttaccgc acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg totcaatatg 250

cccctcttg catatcatat ttggaggat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaa tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggt ccagttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa gtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcattttggt ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggtttc ctcactgtgc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaacaat atataaaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaattgtgt 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5					10				15	
Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25				30	
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40				45	
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55				60	
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70				75	
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85				90	
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100				105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50

tgtaataccc tgaatcccct tgtactccca gactacctca tccacgcttt 100

cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150

atatgcccct cttggcatat catatttggg ggtatatgag tagaccagtg 200

atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250

tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300

tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350

tagaacaaca cacagaagaa ttggtccagt taagtgcatt caaaaagcca 400

ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450

gaatctgata agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaatt tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggacccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagagggttg caggctgttt 300
tcaatttgtc agtttgtgga tgatggaatt gacttaaatt gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500
 aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
 gttatatcc agtctaagcc agaaatccag tacgcaccac atttggagca 650
 ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgct ctctcgggtga tggattgct ttggatttgt tgtgcaactg 850
 ttgctacagc tgtggagcag tatgttcct ctgagaagct gagtatctat 900
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
 caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25				30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40				45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55				60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70				75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85				90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100				105	

Gln Ser Asp Glu	Gln Tyr Ala Cys His	Leu Gly Cys Gln Asn Gln
110		115 120
Leu Pro Phe Ala	Glu Leu Arg Gln Glu	Gln Leu Met Ser Leu Met
125		130 135
Pro Lys Met His	Leu Leu Phe Pro Leu	Thr Leu Val Arg Ser Phe
140		145 150
Trp Ser Asp Met	Met Asp Ser Ala Gln	Ser Phe Ile Thr Ser Ser
155		160 165
Trp Thr Phe Tyr	Leu Gln Ala Asp Asp	Gly Lys Ile Val Ile Phe
170		175 180
Gln Ser Lys Pro	Glu Ile Gln Tyr Ala	Pro His Leu Glu Gln Glu
185		190 195
Pro Thr Asn Leu	Arg Glu Ser Ser Leu	Ser Lys Met Ser Tyr Leu
200		205 210
Gln Met Arg Asn	Ser Gln Ala His Arg	Asn Phe Leu Glu Asp Gly
215		220 225
Glu Ser Asp Gly	Phe Leu Arg Cys Leu	Ser Leu Asn Ser Gly Trp
230		235 240
Ile Leu Thr Thr	Thr Leu Val Leu Ser	Val Met Val Leu Leu Trp
245		250 255
Ile Cys Cys Ala	Thr Val Ala Thr Ala	Val Glu Gln Tyr Val Pro
260		265 270
Ser Glu Lys Leu	Ser Ile Tyr Gly Asp	Leu Glu Phe Met Asn Glu
275		280 285
Gln Lys Leu Asn	Arg Tyr Pro Ala Ser	Ser Leu Val Val Val Arg
290		295 300
Ser Lys Thr Glu	Asp His Glu Glu Ala	Gly Pro Leu Pro Thr Lys
305		310 315
Val Asn Leu Ala	His Ser Glu Ile	
320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtcag agagggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatacga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
cacactggcc ggatctttta gaggcctttg accttgacca agggctcngga 50
aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100
cgaagggagc ctttgggtga ggaccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggcttgcc ggaggttcgg ggaccgcttc ggctgaagca 200
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagaggttg caggctgttt tcaatttgtc agtttggtga tgatggaatt 350
gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550
gatggactcc gc 562

<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg cgggaggttc ggggaccgct tcggctgaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cggccccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccgaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggcttc tgggtcaaggg 850
 acaagtgaag agaacacttt ttacagttgg ctagaagggtc tctgtgtaga 900
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950
 tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
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 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatgtt 1200
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 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300
 gactttcgac tgcatttttag aaatatattca agaattatgg attgtgttgg 1350
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 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450
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 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550
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 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650
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 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaaag taatacttta ataatgtggt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaata 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
1				5					10					15

Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
				20				25						30

Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp		35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg		50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg		65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp		80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln		95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr		110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu		125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys		140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe		155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp		170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp		185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys		200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln		215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu		230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His		245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu		260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln		275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg		290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu		305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100

nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150

ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200

caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250

attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300

tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtggtacca ttcttngagc gcccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcac ttcttttgca ttttgatgag aattcatttt 500
tttgctg 507

<210> 339

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

aagctgccgg agctgcaatg 20

<210> 340

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 340

ttgcttctta atcctgagcg c 21

<210> 341

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

aaaggaggac tttcgactgc 20

<210> 342

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

agagattcat ccaactgctcc aagtcg 26

<210> 343

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtgggta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcgacg cgtgggttg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggactttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
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gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agaggggtgg ggcagtgtct ctgaagggtcc ataaaagaaa 550
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gcctccttca actgggagca tgttctgagg gtgcctccc aagcctggga 700
gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
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gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
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aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
<211> 124
<212> PRT
<213> Homo sapiens

<400> 346
Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
1 5 10 15
Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
20 25 30
Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
35 40 45
Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
50 55 60
Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
65 70 75
Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
80 85 90
Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
95 100 105
Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
110 115 120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
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ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgtcct 200
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatgtt 300
gggggtggac agcgatggat gctggtgggc gcccctggg atgggccttc 350
aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcgtcactc acctgttctt gcccctgggtg ttcct 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
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catctggggtt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttattttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
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ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctgggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
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ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950
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cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
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 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
 ctctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
 aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
 gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350
 gtctaacaga aactgactg aggcttaggg gatgtgacct ctagactggg 1400
 ggctgccact tgctggctga gcaacctgg gaaaagtgaac ttcattccctt 1450
 cggtcctaag ttttctcatt tgtaattggg gaattacctt cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacaccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact gggtggttg gagagccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttg taaagtacag 2000
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 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1				5				10					15	

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
			20					25					30	

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcaca tggttctaga agaaatctgg acaagtcttt 250
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450
tggatcccca gcagctggtg ctcaactcact gaaggctcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
agaaactcaa ccataccttac ccgacctggg atggagatca ccaaagatgg 650
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaacccttg cgccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgccacgcg tccgagggac aagagagaag agagactgaa 50
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ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaaagg agagagggag gaggaggagg agatgcggga 200
tgagagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaaggcg gatctcagtc cctggctgct ttggcatttg 450
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500
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gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
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 tgtggagctg aagaggggttc tttatgaccc ctttctgccc ccattaaggc 850
 tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900
 catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950
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 ctgcgcacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050
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 gtcctaagcc tccccacaag gcgaggggag ttacccttaa aacaaagcta 1650
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
1				5					10					15

Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
				20					25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
				50					55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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ccgccagcct ccgccgccga gctcgttcg tgtccccgcc cctcgtcct 100
gcagctactg ctcagaaacg ctggggcgcc caccctggca gactaacgaa 150
gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250
ctgcagtcag caccacgtc gccccggac gctcggtgct caggcccttc 300
gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350
cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400
ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450
atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550
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gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650
catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700
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cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850
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agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000
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 attttttttc tgctggtgga ttacatatt aaattttttc tgctggtgga 3000
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
1				5				10					15	

Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu		35	40	45
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn		50	55	60
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln		65	70	75
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val		80	85	90
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp		95	100	105
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu		110	115	120
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln		125	130	135
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His		140	145	150
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys		155	160	165
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly		170	175	180
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile		185	190	195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly		200	205	210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser		215	220	225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys		230	235	240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu		245	250	255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His		260	265	270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser		275	280	285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg		290	295	300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala		305	310	315

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100
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ggccagcgcc ctccccatgt ccctgctccc acgcccgcgc cctccggta 200
gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250
accgcgcgtg tggacgggtc caaatgcaag tgctcccgga agggacccaa 300
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtac 400
cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450
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agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550
gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650
attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700
gcgtgcgaaa ggcttcaga tgggagaccc atctctcttg tgctccagac 750
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cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950
gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000
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ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100
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agatcctgtg atggcgagac aaatgatcct taaagaaggt gtgggggtctt 1200
tcccaacctg aggatttctg aaagggtcac aggttcaata tttaatgctt 1250
cagaagcatg tgaggttccc aacactgtca gcaaaaacct taggagaaaa 1300
cttaaaaata tatgaataca tgcgcaatac acagctacag acacacattc 1350
tgttgacaag ggaaaacctt caaagcatgt ttctttccct caccacaaca 1400
gaacatgcag tactaaagca atatatttgt gattcccat gtaattcttc 1450
aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgogccc 1500
tttctctgtg acatataccc ttaagaacgc cccctccaca cactgcccc 1550
cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600
aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650
ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu	
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20					25					30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys	
				35					40					45	
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	
				50					55					60	
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val	
				65					70					75	
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	
				80					85					90	
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	
				95					100					105	
Arg	Arg	Val	Tyr	Glu	Glu										
				110											

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373
ctccgggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374
<211> 3113
<212> DNA
<213> Homo sapiens

<400> 374
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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150
caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200
tggagcagta cttaggggtc ccctatgcct cacccccac tggagagagg 250
cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300
tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350
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acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450
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gtaatgaccg tggatgaagac gaagatatc atgatcagaa cagtaagaag 550
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cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900
cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950
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atcatgctgg gcgtcaacca aggggaaggc ctgaagtctg tggacggcat 1200

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aggaccctca caaacacagg cctgaggaca caactgtcct cattgaaacc 2050
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 taagagactt tgt 3113

<210> 375
 <211> 816
 <212> PRT
 <213> Homo sapiens

<400> 375
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 Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn
 20 25 30
 Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn
 35 40 45
 Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala
 50 55 60
 Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro
 65 70 75
 Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val
 80 85 90
 Cys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu
 95 100 105
 Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val
 110 115 120
 Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro
 125 130 135
 Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr
 140 145 150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser	155	160	165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu	170	175	180
Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly	185	190	195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly	200	205	210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu	215	220	225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly	230	235	240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly	245	250	255
Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser	260	265	270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu	275	280	285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile	290	295	300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met	305	310	315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln	320	325	330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile	335	340	345
Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu	425	430	435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
				800					805					810
His	Ser	Thr	Thr	Arg	Val									
				815										

<210> 376

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

ggcaagctac ggaaacgtca tcgtg 25

<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100
ttgttggggc ctgggcaggc gccacagcaa gtcggggcgg gtcaaacgtt 150
cgagtacttg aaacgggagc actcgtctgc gaagccctac caggggtgtgg 200
gcacaggcag ttcctcactg tggaatctga tgggcaatgc catggtgatg 250
accagtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300
gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg caggtgcact 350
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atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaacat 450
ggacaaatth gtggggctgg gagtatttgt agacacctac cccaatgagg 500
agaagcagca agagcgggta tccccctaca tctcagccat ggtgaacaac 550
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<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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Arg	Cys	Leu	Ser	Ala	Arg	Asp	Gly	Ser	Arg	Met	Leu	Leu	Leu	Leu
				20					25					30

Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly		35	40	45
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro		50	55	60
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met		65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp		80	85	90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe		95	100	105
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln		110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr		125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys		140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu		155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn		170	175	180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr		185	190	195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp		200	205	210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met		215	220	225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val		230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser		245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys		260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu		275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro		290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe		305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ccttgggtcg tggcagcagt gg 22

<210> 382
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
cactctccag gctgcatgct cagg 24

<210> 383
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
gtcaaacggt cgagtacttg aaacggggagc actcgctgtc gaagc 45

<210> 384
<211> 3150
<212> DNA
<213> Homo sapiens

<400> 384
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gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100
ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150
tgggggtctgg ctcagaattc ctgcagctgg tgaaaatctg ttttctagaa 200

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cattgtgtga gatgggagag ctacacaga caggagtgtg gcagcatttg 800
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ttctcccaag cccatgtgcc cgcttgaaaa cttgggtccgc tttgtgaaaa 1650

gggacatggt tgtagccctg ggtggcagtg gtacaaatta ttatgatgca 1700
tgtcacaggg aaggattcta aaaggatatgc agtacagcag tatagaatcc 1750
atgccaatag agagcatagg gaaagggtcca cttctagttt tgtctgttac 1800
taagggtaga agattattgc tttttaaagg ctaaattattg tttgtgggaa 1850
ccacagatgg ttgggggtga acagtaagca cattgctgca atgtggtacg 1900
tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggactt 1950
tatcatagcc agacttcgct tagaatgcca gaataatata gttcaagacc 2000
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tgtgatggaa ccagcacacc tcaacaaaaa tttttttaat cttagacatt 2100
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gtgttgcatc tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala
1 5 10 15

Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile
20 25 30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
95 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe
215 220 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
230 235 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

aaaaaagctc actaaagttt ctattagagc gaatacggta gattttccatc 50

cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100

atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150

gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250

gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300

gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350

aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400

aaagggttg tctgtctggg aatcctcctg gggactctgt gggagaccgg 450

atgcacccag atacgtatt cagttccgga agagctggag aaaggctcta 500

gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550

gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgccct 600

gaatccgcgc agcggcagct tggtcacggc gggcaggata gaccgggagg 650

agctctgtat gggggccatc aagtgtcaat taaatctaga cattctgatg 700
gaggataaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750
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acaccatcca aggggcaagc ctatcgtcct acgtgtccat caactccgac 1900
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 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggaggtt 3250
 gcaatgagct gagattgtgc cattgcactc cagcctgggc aacaagagtg 3300
 aaactctatc tca 3313

<210> 390
 <211> 916
 <212> PRT
 <213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu		1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln		20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val		35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala		50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe		65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile		80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn		95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu		110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu		125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met		140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn		155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu		170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val		185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu		200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr		215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro		230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu		245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp		260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp		275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcg ccaagacgtg 200
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
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 caagaaatac ctgtggttca gtccatccca caccctgct acaacagcag 500
 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
 aggcattcct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
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<210> 395
 <211> 260
 <212> PRT
 <213> Homo sapiens

<400> 395
 Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
 1 5 10 15
 Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
 20 25 30
 Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
 35 40 45
 Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
 50 55 60
 Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
 65 70 75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccgccc gggcccgcg ccgcgcccgc gccaggtga gcgctccgcc 150
cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200
ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250
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 cccggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000
 acaacgcgct gcaggcactg cctgatgaca ccttccgcga cctggggaac 1050
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<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala	
				20					25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
				35					40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
				50					55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
				65					70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
				80					85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
				95					100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
				110					115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
				125					130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
				140					145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
				155					160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
				170					175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
				185					190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
				200					205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
				215					220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
				230					235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
				245					250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
				260					265					270	

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser Glu Val	
275		280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys Arg	
290		295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr Gly Pro	
305		310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu Pro Leu	
320		325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335		340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350		355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365		370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380		385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395		400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410		415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425		430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440		445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455		460	465
Leu Trp Thr Val	Leu Gly Pro Cys		
470			

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgccct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400
gctcaatcag gagaccgcg atttgttgct aaatgagaaa ttggaccgtg 450
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500
ctagagagtc ctttcgagtt ttttcaagct gagctgcaag taatagacat 550
aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600
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<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu	1	5	10	15
Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu	20	25	30	
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe	35	40	45	
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe	50	55	60	
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His	65	70	75	
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys	80	85	90	
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu	95	100	105	
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala	110	115	120	
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu	125	130	135	
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly	140	145	150	

Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440	445	450	
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455	460	465	
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470	475	480	
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485	490	495	
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500	505	510	
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515	520	525	
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530	535	540	
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545	550	555	
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560	565	570	
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575	580	585	
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590	595	600	
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605	610	615	
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620	625	630	
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635	640	645	
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650	655	660	
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665	670	675	
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680	685	690	
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695	700	705	
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710	715	720	

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
 cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
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 acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
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 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500
 cacttccctg acagagaaga ggagtattac acagagccag aagtggcggg 550
 atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
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<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

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				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
				155					160					165
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

	260		265		270
Ala Lys Pro Met	Ala Arg Phe Asn His	Thr Asp Arg Thr Leu Glu			
	275	280		285	
Thr Leu Lys Ile	Phe Ile Phe Asn Gln	Thr Gly Ile Glu Ala Lys			
	290	295		300	
Lys Asn Val Val	Val Thr Gln Ala Asp	Gln Ile Gly Pro Leu Pro			
	305	310		315	
Ser Thr Leu Ile	Lys Ser Val Asp Trp	Leu Leu Val Phe Ser Leu			
	320	325		330	
Phe Phe Leu Ile	Ser Phe Ile Met Tyr	Ala Thr Ile Arg Thr Glu			
	335	340		345	
Ser Ile Arg Trp	Leu Ile Pro Gly Gln	Glu Gln Glu His Val Glu			
	350	355		360	

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tcctgtttta caccccgtag tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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gcgcagcaat tgcaagccca tcccgggtcaa cctgcagctg tgccacggca 200
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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

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His Cys Cys Leu Gly	Ser Ala Arg Gly	Leu Phe Leu Phe Gly	Gln
20		25	30
Pro Asp Phe Ser Tyr	Lys Arg Ser Asn Cys	Lys Pro Ile Pro Val	
35		40	45
Asn Leu Gln Leu Cys	His Gly Ile Glu Tyr	Gln Asn Met Arg Leu	
50		55	60
Pro Asn Leu Leu Gly	His Glu Thr Met Lys	Glu Val Leu Glu Gln	
65		70	75
Ala Gly Ala Trp Ile	Pro Leu Val Met Lys	Gln Cys His Pro Asp	
80		85	90
Thr Lys Lys Phe Leu	Cys Ser Leu Phe Ala	Pro Val Cys Leu Asp	
95		100	105
Asp Leu Asp Glu Thr	Ile Gln Pro Cys His	Ser Leu Cys Val Gln	
110		115	120
Val Lys Asp Arg Cys	Ala Pro Val Met Ser	Ala Phe Gly Phe Pro	
125		130	135
Trp Pro Asp Met Leu	Glu Cys Asp Arg Phe	Pro Gln Asp Asn Asp	
140		145	150
Leu Cys Ile Pro Leu	Ala Ser Ser Asp His	Leu Leu Pro Ala Thr	
155		160	165
Glu Glu Ala Pro Lys	Val Cys Glu Ala Cys	Lys Asn Lys Asn Asp	
170		175	180
Asp Asp Asn Asp Ile	Met Glu Thr Leu Cys	Lys Asn Asp Phe Ala	
185		190	195
Leu Lys Ile Lys Val	Lys Glu Ile Thr Tyr	Ile Asn Arg Asp Thr	
200		205	210
Lys Ile Ile Leu Glu	Thr Lys Ser Lys Thr	Ile Tyr Lys Leu Asn	
215		220	225
Gly Val Ser Glu Arg	Asp Leu Lys Lys Ser	Val Leu Trp Leu Lys	
230		235	240
Asp Ser Leu Gln Cys	Thr Cys Glu Glu Met	Asn Asp Ile Asn Ala	
245		250	255
Pro Tyr Leu Val Met	Gly Gln Lys Gln Gly	Gly Glu Leu Val Ile	
260		265	270
Thr Ser Val Lys Arg	Trp Gln Lys Gly Gln	Arg Glu Phe Lys Arg	
275		280	285
Ile Ser Arg Ser Ile	Arg Lys Leu Gln Cys		

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
cctcacaggt gcactgcaag ctgtc 25

<210> 418
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
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<210> 419
<211> 1830
<212> DNA
<213> Homo sapiens

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gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
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<210> 420
<211> 560
<212> PRT
<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg
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Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val
				110					115					120
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu
				125					130					135
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu
				140					145					150
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met
				155					160					165
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val
				170					175					180
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met
				185					190					195
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser
				200					205					210
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala
				215					220					225
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys
				230					235					240
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys
				245					250					255

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala	Leu Leu
260		265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly
275		280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu
290		295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala
305		310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe
320		325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala
335		340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val
350		355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly
365		370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile
380		385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu
395		400	405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp	Trp
410		415	420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe	Ser
425		430	435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu	Gln
440		445	450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly	Gly
455		460	465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg	Ala
470		475	480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala	Arg
485		490	495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His	Pro
500		505	510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala	Thr
515		520	525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln	Ala
530		535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
560

<210> 421
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
agcttctcag ccctcctgga gcag 24

<210> 422
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 422
cggttcaata aacctggacg cttgg 25

<210> 423
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 423
tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424
<211> 4313
<212> DNA
<213> Homo sapiens

<400> 424
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aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250
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 aaaaaaaaaa aaa 4313

<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met Met Gln Leu Leu Gln Leu Leu Leu Gly Leu Leu Gly Pro Gly
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Gly Tyr Leu Phe	Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr	Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala	Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val	Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp	Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln	Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu	His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val	Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val	Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305	310	315
Pro Ala Tyr Glu Val	Asp Val Gln Ala Arg Asp Leu Gly Pro Asn	
320	325	330
Pro Ile Pro Ala His	Cys Lys Val Leu Ile Lys Val Leu Asp Val	
335	340	345
Asn Asp Asn Ile Pro	Ser Ile His Val Thr Trp Ala Ser Gln Pro	
350	355	360
Ser Leu Val Ser Glu	Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu	
365	370	375
Val Met Ala Asp Asp	Leu Asp Ser Gly His Asn Gly Leu Val His	
380	385	390
Cys Trp Leu Ser Gln	Glu Leu Gly His Phe Arg Leu Lys Arg Thr	
395	400	405
Asn Gly Asn Thr Tyr	Met Leu Leu Thr Asn Ala Thr Leu Asp Arg	
410	415	420
Glu Gln Trp Pro Lys	Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln	
425	430	435
Gly Leu Gln Pro Leu	Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile	
440	445	450
Ser Asp Ile Asn Asp	Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr	
455	460	465
Glu Val Ser Thr Arg	Glu Asn Asn Leu Pro Ser Leu His Leu Ile	
470	475	480
Thr Ile Lys Ala His	Asp Ala Asp Leu Gly Ile Asn Gly Lys Val	
485	490	495
Ser Tyr Arg Ile Gln	Asp Ser Pro Val Ala His Leu Val Ala Ile	
500	505	510
Asp Ser Asn Thr Gly	Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr	
515	520	525
Glu Glu Met Ala Gly	Phe Glu Phe Gln Val Ile Ala Glu Asp Ser	
530	535	540
Gly Gln Pro Met Leu	Ala Ser Ser Val Ser Val Trp Val Ser Leu	
545	550	555
Leu Asp Ala Asn Asp	Asn Ala Pro Glu Val Val Gln Pro Val Leu	
560	565	570
Ser Asp Gly Lys Ala	Ser Leu Ser Val Leu Val Asn Ala Ser Thr	
575	580	585

Gly His Leu Leu Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	590	595	600
Ala Gly Thr Asp Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	605	610	615
Phe Leu Leu Thr Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	620	625	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	635	640	645
Leu Phe Ile Leu Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val	650	655	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile	665	670	675
Val Val Glu Asp Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	680	685	690
Leu Arg Val Met Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser	695	700	705
Ala Arg Lys Pro Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile	710	715	720
Cys Leu Ala Val Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	725	730	735
Phe Met Ser Ile Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	740	745	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	755	760	765
Pro Gln Lys His Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val	770	775	780
Leu Arg Gly Gln Ala Gly Glu Pro Cys	Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met	Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg Thr	815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu	Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln Pro	860	865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaagacag gccaggatcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctcca gatactattt 200

tttgatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250

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 aaaaaaaaaa agggcggccg cgactctaga gtcgacctgc agaagcttgg 2000
 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

Met	Ser	Phe	Leu	Ile	Asp	Ser	Ser	Ile	Met	Ile	Thr	Ser	Gln	Ile	1	5	10	15
Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe	20	25	30	
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser	35	40	45	
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe	50	55	60	
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp	65	70	75	
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val	80	85	90	
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu	95	100	105	
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe	110	115	120	
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser	125	130	135	
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val	140	145	150	
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly	155	160	165	
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn	170	175	180	
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln				

185										190					195				
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala					
				200						205					210				
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser					
				215						220					225				
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly					
				230						235					240				
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu					
				245						250					255				
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala					
				260						265					270				
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr					
				275						280					285				
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys					
				290						295					300				
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys					
				305						310					315				
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu					
				320						325					330				
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe					
				335						340					345				
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu					
				350						355					360				
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser					
				365						370					375				
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr					
				380						385					390				
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu					
				395						400					405				
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn					
				410						415					420				
Phe	Tyr	His	Arg	Trp	Phe	Asp	Val	Ile	Phe	Leu	Val	Ser	Ala	Leu					
				425						430					435				
Ser	Ser	Ile	Leu	Phe	Leu	Tyr	Leu	Ala	His	Lys	Gln	Ala	Pro	Glu					
				440						445					450				
Lys	Gln	Met	Ala	Pro															
				455															

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

<400> 431
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ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgtta 250
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tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
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tctgctgac ctggttttca tggtgccttt ttacattggc tattttattg 350
tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tgtgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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ttctcacggg ctgtgcctt caatctggac gtgatgggtg ccttgcgcaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccag agctggctgc tgggtgggtgc tccccaggcc 250

ctggctcttc ctgggcagca ggcgaatgc actggaggcc tcttcgcttg 300

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a 3951

<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
			20						25					30

Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45

Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90

Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105

Val Asp Ile Asp	Gln Gly Ala Asp Met	Gln Lys Glu Ser Lys Glu
110	115	120
Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly Gly
125	130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg Val
140	145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe Val
155	160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly Glu
170	175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe Gly
185	190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser His
200	205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly Thr
215	220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala His
230	235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln Asp
245	250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe Ser
260	265	270
Ile Asp Ser Gly	Lys Gly Leu Val Arg	Ala Glu Glu Leu Ser Phe
275	280	285
Val Ala Gly Ala	Pro Arg Ala Asn His	Lys Gly Ala Val Val Ile
290	295	300
Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met Leu
305	310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala Val
320	325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly Ala
335	340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val Tyr
350	355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro Leu
365	370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu Ala
380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly	680	685	690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	695	700	705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met	710	715	720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro	725	730	735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val	740	745	750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr	755	760	765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr	770	775	780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu	785	790	795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro	800	805	810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser	815	820	825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val	830	835	840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln	845	850	855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro	860	865	870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val	875	880	885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser	890	895	900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg	905	910	915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu	920	925	930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu	935	940	945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn	950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100
ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgcagctg 200
ccgcggcggt ggctgcagcc ggggggcggt cggacggcgg taattttctg 250
gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300
acagtgaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
aagcagtgcc cagtgggtct tcccagccct gtttgtggtt cagatggtca 600
tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650
aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tgtaagaga gcatgcagtg acctggagtt 750
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gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
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gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950
 tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000
 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
 ctactgcttc cagagacagc aagaccacc ttgccagact gagctcagca 1100
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 ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200
 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250
 gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300
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 gggatgatga tgatgggtgg gatgacctg atgtatacat ttgattgatg 1450
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 cctatttaaa attatcttct tcccataaa caaatgatt ctaaacctca 1550
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 aattctaagt gaaatttaaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatagc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp
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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20				25						30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

	320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly	335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp	350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn	365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe	380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu	395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu	410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr	425	430	435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

cagactccag atttcctgt caaccacgag gagtccagag aggaaacgcg 50
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gctctgctc cgggtgctgct gcctggggcg gccggcttca caccttccct 200
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accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300
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 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
ctctgaaaaa ctggtgtctg tgctcagtgg ggctgagga tccttcgtgt 350
cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500
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gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650
gctcatcatg gacatgagac cagtgtgaag actcacctg gaagagaata 700
ttctcccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750
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aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
				20					25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
				35					40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
				50					55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
				65					70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
				80					85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
				95					100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
				110					115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
				125					130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
				140					145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
				155					160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
				170					175						

<210> 453
<211> 550
<212> DNA
<213> Homo sapiens

<400> 453

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ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgcccggccc 150
tgcgctgcta cgtctgtccg gagcccacag gagtgtcggg ctgtgtcacc 200
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400
tctgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
tccgactgta gagtccccgc ccacccccat ggcctatgc ggcccagccc 500
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454

<211> 125

<212> PRT

<213> Homo sapiens

<400> 454

Met	Arg	Gly	Thr	Arg	Leu	Ala	Leu	Leu	Ala	Leu	Val	Leu	Ala	Ala
1				5					10					15

Cys	Gly	Glu	Leu	Ala	Pro	Ala	Leu	Arg	Cys	Tyr	Val	Cys	Pro	Glu
			20						25					30

Pro	Thr	Gly	Val	Ser	Asp	Cys	Val	Thr	Ile	Ala	Thr	Cys	Thr	Thr
				35					40					45

Asn	Glu	Thr	Met	Cys	Lys	Thr	Thr	Leu	Tyr	Ser	Arg	Glu	Ile	Val
				50					55					60

Tyr	Pro	Phe	Gln	Gly	Asp	Ser	Thr	Val	Thr	Lys	Ser	Cys	Ala	Ser
				65					70					75

Lys	Cys	Lys	Pro	Ser	Asp	Val	Asp	Gly	Ile	Gly	Gln	Thr	Leu	Pro
				80					85					90

Val	Ser	Cys	Cys	Asn	Thr	Glu	Leu	Cys	Asn	Val	Asp	Gly	Ala	Pro
				95					100					105

Ala	Leu	Asn	Ser	Leu	His	Cys	Gly	Ala	Leu	Thr	Leu	Leu	Pro	Leu
				110					115					120

Leu	Ser	Leu	Arg	Leu
				125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150

gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caactaccag ccgtaccogt gcgcagagga 400
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450
 acgcaggcgt gcaaatctgt ctgcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
 tctggtccaa gatctgtaaa cctgtcctga aagaaggta agtgtgtacc 800
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttgta 850
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ctttttatga 1000
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100
 ttatggaact cccctgtgat tgcagtaaat tactgtattg taaattctca 1150
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta ttttctaaa 1200
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 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaatca 1300
 tttcagctta tagttcttaa aagcataacc ctttaccoca ttttaattcta 1350
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 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
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 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala	
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser	
				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
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ttttgcagcg gaacgggaag gttttgtggg acccaggttg aaatgacggt 100
catttttttt tctttctcct tcnggagtc tnttgagang atggtttttg 150
gcgcagcggg agctaaccgc gttttttgtn gcgatggtag cggcggtttt 200
cggcggccac ctnttgctgg gagtgagcgc caccttgaat cggttttcaa 250
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angcgggcgt gcaaantgt ntngcctgca ggaagcgccg aaaacgctgc 500
atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

<400> 458
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gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200
gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250
ttcacagatt aatatTTTTg gggacagatt tgtgatgctt gattcacct 300

tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350
accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaag 400
agaatgggag tctggttaaa taaagatgac tatatcagag acttgaaaag 450
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500
atcaggatth ttacagthta cttggagtgt ccaaaactgc aagcagtaga 550
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ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750
ctattatcgt tatgattttg gtattttatga tgatgatcct gaaatcataa 800
cattggaaag aagagaatth gatgctgctg ttaattctgg agaactgtgg 850
tttgtaaatt tttactcccc aggctgttca cactgccatg atttagctcc 900
cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950
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tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900
atcttggagt tcatagagga tcttatgaat ccttcagtgg tctcccttac 1950
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ggatgggtga tttctattct ccgtgggtgc atccttgcca agtcttaatg 2050
ccagaatgga aaagaatggc ccggacatta actggactga tcaacgtggg 2100
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tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650
tgttgaagat gaagaaaaag tttaaaagaa attctgacag atgacatcag 2700
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aacgattctt agctcagagc catacaaaag taggctggat tcagtccatg 3000
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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys
1				5					10				15	

Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val
			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40					45

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55					60

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70					75

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly		380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val		395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn		410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro		425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu		440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His		455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr		470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His		485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro		500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr		515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro		530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met		545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys		560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr		575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln		590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg		605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr		620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp		635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
				725					730					735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
				740					745					

<210> 460
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
 actccccagg ctgttcacac tgcc 24

<210> 461
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 461
 gatcagccag ccaataccag cagc 24

<210> 462
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 462
 gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

agacagtacc tcctccctag gactacacaa ggactgaacc agaaggaaga 50
ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100
caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250
attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300
agtgccgaaa actaggcgtc actgcgcgtg cgtatgtggt agactgcagc 350
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgac 450
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500
ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550
aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600
ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt 650
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700
aacctcatgt ctctgcccag tttttgtgaa tactgggttc accaaaaatc 750
caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800
ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900
cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950
aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000
ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050
tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100
caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150
gtagtttttc ataggtctgt ttttcctttc atgcctctta aaaacttctg 1200
tgcttacata aacatactta aaagggttttc tttaagatat tttatttttc 1250
catttaaagg tggacaaaag ctacctccct aaaagtaaata acaaagagaa 1300
cttatttaca caggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450
 attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550
 aactctgaag tccacaaaaa gtggaccctc tatatttcct ccctttttat 1600
 agtcttataa gatacattat gaaaggtgac cgactctatt ttaaacttca 1650
 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700
 ttcatatatc cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met	Asn	Ile	Ile	Leu	Glu	Ile	Leu	Leu	Leu	Ile	Thr	Ile	Ile	
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Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg
				20				25					30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly
				35				40					45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln
				50				55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu
				65				70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr
				80				85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn
				95				100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn
				110				115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu
				125				130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp
				140				145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly

	155		160		165
His Ile Val Thr	Val Ala Ser Val Cys	Gly His Glu Gly Ile	Pro		
	170	175	180		
Tyr Leu Ile Pro	Tyr Cys Ser Ser Lys	Phe Ala Ala Val Gly	Phe		
	185	190	195		
His Arg Gly Leu	Thr Ser Glu Leu Gln	Ala Leu Gly Lys Thr	Gly		
	200	205	210		
Ile Lys Thr Ser	Cys Leu Cys Pro Val	Phe Val Asn Thr Gly	Phe		
	215	220	225		
Thr Lys Asn Pro	Ser Thr Arg Leu Trp	Pro Val Leu Glu Thr	Asp		
	230	235	240		
Glu Val Val Arg	Ser Leu Ile Asp Gly	Ile Leu Thr Asn Lys	Lys		
	245	250	255		
Met Ile Phe Val	Pro Ser Tyr Ile Asn	Ile Phe Leu Arg Leu	Gln		
	260	265	270		
Lys Phe Leu Pro	Glu Arg Ala Ser Ala	Ile Leu Asn Arg Met	Gln		
	275	280	285		
Asn Ile Gln Phe	Glu Ala Val Val Gly	His Lys Ile Lys Met	Lys		
	290	295	300		

<210> 465

<211> 1547

<212> DNA

<213> Homo sapiens

<400> 465

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gagaggggccc agcccgcccg gggcaggatg accaaggccc ggctgttccg 150

gctgtggctg gtgctggggt cgggtgtcat gatcctgctg atcatcgtgt 200

actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250

aggccgcaca cggggccgccc gctgcccacg cccgggcccg acagggacag 300

ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350

gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400

cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450

gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500

ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550

aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650
gcaccaactg gaagcgctg atgatcgtgc tgagcggaag cctgctgcac 700
cgcggtgcgc cctaccgca cccgctgcgc atcccgcgcg agcacgtgca 750
caacgccagc ggcacactga cttcaacaa gttctggcgc cgctacggga 800
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850
ctcttcgtgc ggcaccctt cgtgcgctg atctccgct tccgcagcaa 900
gttcgagctg gagaacgagg agttctaccg caagtctgcc gtgcccattg 950
tgcggtgtga cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000
ttccgcgctg gctcaagggt gtccttcgcc aacttcatcc agtacctgct 1050
ggaccgcgac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100
tgtaccgct ctgccaccg tgccagatcg actacgactt cgtggggaag 1150
ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200
ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250
gctgggagga ggactgggtc gccaagatcc ccctggcctg gaggcagcag 1300
ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350
cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgctg 1400
cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450
gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500
atcgatattg ttttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
				20					25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
				50					55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser
				65					70					75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln
				80					85					90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp
				95					100					105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln
				110					115					120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser
				125					130					135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro
				140					145					150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala
				155					160					165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg
				170					175					180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro
				185					190					195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala
				200					205					210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys
				215					220					225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys
				230					235					240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe
				245					250					255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe
				260					265					270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro
				275					280					285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe
				290					295					300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu
				305					310					315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His
				320					325					330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu
				335					340					345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
 tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50
 ctttgagggt gaaagaggcc cagagtagag agagagagag accgacgtac 100
 acgggatggc tacgggaacg cgctatgccg ggaagggtgg ggtcgtgacc 150
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccaccaccc ccacagaggc 400
 ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaacct 450
 ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500
 tcaagggaat gtcataca tctccagcct ggtgggggca atcggccagg 550
 cccaggcagt tcctatgtg gccaccaagg gggcagtaac agccatgacc 600
 aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
 ggccgcatgg gccagcccgc tgaggctggg gctgcggcag tgttcctggc 800
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

cccgatatcc cttcctgatt tctctcattt ctacttgggg cccccttcct 950
 aggactctcc caccaccaaac tccaacctgt atcagatgca gcccacaagc 1000
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggtc 1050
 ccataaaaac gatttgcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr
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Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn
				125					130					135
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln
				140					145					150
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr
				155					160					165
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn
				170					175					180
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu
				185					190					195
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met
				200					205					210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
 aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agcccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgacgct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgcg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
 gccaggccag cagcccagaa ccctcctcct tgcacctttg tgccaagaaa 650
 ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
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 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
				35					40					45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
				155					160					165
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
				170					175					180

<210> 471
 <211> 2368
 <212> DNA
 <213> Homo sapiens

<400> 471
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 aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100
 ctccccgccg agaagcctcg ctcggcgccc aacatggcgg gtgggcgctg 150
 cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
 cagcccatga ccgcctcaa ctggacgctg gtgatggagg gcgagtggat 300
 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttatt 500

gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
gatgtctgga atggctggtc tttttagcat ctctggcaag atatggcatc 650
ttcacaacta tttcacagtg actcttggaa ttcttgcttg gtgttcttat 700
gtgtttttcg tcatagccac cttggttttt ggccttttta tgggtctggg 750
cttgggtgga atatcagaat gtttctatgt gccacttcca aggcatttat 800
ctgagcggtc tgagcagaat cggagatcag aggaggctca tagagctgaa 850
cagttgcagg atgcggagga ggaaaaagat gattcaaag aagaagaaaa 900
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctgggtg 1000
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050
tgtgaccgg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100
agcaaccctg cccagctgac acagaggtgg tggaagactc cttgaggcag 1150
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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser	35	40	45	
Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr	50	55	60	
Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu	65	70	75	
Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys	80	85	90	
Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val	95	100	105	
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg	110	115	120	
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile	125	130	135	
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys	140	145	150	
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser	155	160	165	

Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr	
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				185					190					195	
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile	
				200					205					210	
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg	
				215					220					225	
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln	
				230					235					240	
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu	
				245					250					255	
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu	
				260					265					270	
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu	
				275					280					285	
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly	
				290					295					300	
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu	
				305					310					315	
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr	
				320					325					330	
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala	
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Asp Lys Gly Leu

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

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<210> 474

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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caggggcaga aagaaaagag ctcccaaattg ctatatctat tcaggggctc 150

tcaagaacaa tggaatatca tcttgattta gaaaatttgg atgaagatgg 200

atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250

tttcagagaa aggatcgtgt gctgcatctc ctccttggcg cctcattgct 300

gtaatttttg gaatcctatg cttggtaata ctggtgatag ctgtggctct 350

gggtaccatg ggggttcttt ccagcccttg tctcctaata tggattatat 400

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attcattttg gataggcctt tctcggcccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650

agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700

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aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800

gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgagggtca 850

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 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477
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 20 25 30
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
 170 175 180
 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195
 Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
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<210> 479
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
acaagtgtct tcccaacctg 20

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
atcctcccag agccatggta cctc 24

<210> 481
<211> 51
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<210> 482
<211> 3819
<212> DNA
<213> Homo sapiens

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<210> 483

<211> 693

<212> PRT

<213> Homo sapiens

<400> 483

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				20					25					30
Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	Asn	Gln	Thr	His	Arg	Ser	Ser
				35					40					45
Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	Arg	Ile	Ser	Ile	Glu	Asn
				50					55					60
Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	Phe	Pro	Ala	Ala	His
				65					70					75
Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe
				80					85					90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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ctgccttgca gaggaaan cn tcgggactac acctcaagt gcacatgaac 100
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cgggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200
cctgcacttc tctgctcac ctgcctttcc tggatggggc tcgaggggta 250
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acgctggtgg ccctggtgga tgtggacaac tatggcccca tcattctggc 400
tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450
gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500
tttctgttca acatgg 516

<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

ggcattggag cagtgctggg tg 22

<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

tggaggccta gatgcggctg gacg 24 .

<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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ggttcaggtc caggttttgc tttgatcctt ttcaaaaact ggagacacag 100
aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250
ccgccgtgag tgagctctca cccagtcag ccaaagagc ctcttcgggc 300
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gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500
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gtttgatgaa agatttgggc ttgaagaccc agaagatgac atatgcaagt 600
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tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700
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cagtgtccat aagggaagaa ctaaagagaa ccgataccat tttctggcca 1100
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catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400

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aaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly
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Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe
				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tcctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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gacctctaca ttccattttg gaagaagact aaaaatggtg tttccaatgt 100

ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200
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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu			
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Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe			
				20					25					30			
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn			
				35					40					45			
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro			
				50					55					60			
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn			
				65					70					75			
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His			
				80					85					90			
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu			
				95					100					105			
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro			
				110					115					120			
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp			
				125					130					135			
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu			
				140					145					150			
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys			
				155					160					165			
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly			
				170					175					180			
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile			
				185					190					195			

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480

Glu Ala Ser Phe	Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp	Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln	His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile	Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu	Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser	Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser	Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu	Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn	Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu	Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu	Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu	Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe	Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn	Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys	Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn	Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser	Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr	Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu	Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Ser	Phe	Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu		770	775	780
His	His	Asn	Arg	Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val		785	790	795
Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr		800	805	810
Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val		815	820	825
Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu		830	835	840
Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val		845	850	855
Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile		860	865	870
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile		875	880	885
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys		890	895	900
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys		905	910	915
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu		920	925	930
Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln		935	940	945
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys		950	955	960
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His		965	970	975
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe		980	985	990
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys		995	1000	1005
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln		1010	1015	1020
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr		1025	1030	1035
Asp	Asn	His	Val	Ala	Tyr	Ser	Gln	Val	Phe	Lys	Glu	Thr	Val			1040	1045	

<210> 497

<211> 4199

<212> DNA

<213> Homo sapiens

<400> 497

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acgctgacaa atttggaggt gctatcacta tctttcaatt ctctttcaca 700
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly
245	250	255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro Cys
260	265	270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln Asn
275	280	285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu Arg
290	295	300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys Val
305	310	315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser Gly
320	325	330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu Ser
335	340	345
Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile Ser
350	355	360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu Arg
365	370	375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro Leu
380	385	390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn Phe
395	400	405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn Leu
410	415	420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val Lys
425	430	435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg His
440	445	450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His Ser
455	460	465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys Ala
470	475	480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe Phe
485	490	495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys Leu
500	505	510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr Glu
515	520	525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	755	760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
Asp Ser Ile Lys Gln Tyr	1040		

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 500
<211> 20
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<220>
<223> Synthetic oligonucleotide probe

<400> 500
atccatgagc ctctgatggg 20

<210> 501
<211> 45
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

<400> 503
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<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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<210> 506
<211> 273
<212> PRT
<213> Homo sapiens

<400> 506

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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45	
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu				

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Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly					
	170		175		180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala					
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu					
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala					
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu					
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu					
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys					
	260		265		270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25				30	

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35				40					45	

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
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Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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20										25					30				
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
				35					40					45					
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
				155					160					165					
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
				170					175					180					
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr					
				185					190					195					
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
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Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

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Glu Thr Ser Ser	Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu				
	320		325		330
His Leu Asn Ser	Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu				
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Glu Met Pro Pro	Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala				
	350		355		360

Glu Ala Glu Lys

<210> 516

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 38, 88, 118, 135, 193, 213, 222

<223> unknown base

<400> 516

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cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200

tcttcacccct ttntctctcc cncctcacaa totatgtcct cgccttcaac 250

atcgt 255

<210> 517

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagt cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcaccgggt ggcctggcta aaccgcagca 350

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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

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				20					25					30	
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<212> DNA

<213> Homo sapiens

<400> 524

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<213> Homo sapiens

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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val	695	700	705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly	710	715	720
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<211> 1285

<212> DNA

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<400> 528

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 cagttccatc ttttttttta aattttttct gcctatttaa agacaaatta 2800
 tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612

Met	Met	Leu	Leu	Val	Gln	Gly	Ala	Cys	Cys	Ser	Asn	Gln	Trp	Leu
1				5					10					15
Ala	Ala	Val	Leu	Leu	Ser	Leu	Cys	Cys	Leu	Leu	Pro	Ser	Cys	Leu
				20					25					30
Pro	Ala	Gly	Gln	Ser	Val	Asp	Phe	Pro	Trp	Ala	Ala	Val	Asp	Asn
				35					40					45
Met	Met	Val	Arg	Lys	Gly	Asp	Thr	Ala	Val	Leu	Arg	Cys	Tyr	Leu
				50					55					60
Glu	Asp	Gly	Ala	Ser	Lys	Gly	Ala	Trp	Leu	Asn	Arg	Ser	Ser	Ile
				65					70					75
Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
				80					85					90
Ile	Ser	Thr	Leu	Asn	Lys	Arg	Asp	Tyr	Ser	Leu	Gln	Ile	Gln	Asn
				95					100					105
Val	Asp	Val	Thr	Asp	Asp	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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aaataagaaa attctcaagg aggacgagct cttgagttag acccaacaag 150
ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcctta 250
cctgatcctg ctcaccgctg gcgctgggct gctgggtggc caagttctga 300
atctgcaggc gcggctccgg gtcctggaga tgtatttcct caatgacact 350
ctggcggtg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400
tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450
aactcacctg ggtccgctc agccatgagc acttgctgca gcgggtagac 500
aacttcactc agaaccaggt gatgttcaga atcaaagggt aacaaggcgc 550
cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
gcccgcggg accacctgct gagaaggag ccaagggggc tatgggacga 650
gatggagcaa caggcccctc gggaccccaa ggcccaccg gagtcaagg 700
agaggcgggc ctccaaggac ccaggggtgc tccagggaag caaggagcca 750
ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800
ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850
gggtctccca ggaagcaaag gggacaggg catgaaagga gatgcaggg 900
tcatggggcc tcctggagcc caggggagta aaggtagctt cgggaggcca 950
ggcccaccag gtttggtggt ttttctgga gctaaaggag atcaaggaca 1000
acctggactg cagggtgttc cgggccctcc tgggtgcagt ggacaccag 1050
gtgccaaggg tgagcctggc agtgctggct ccctgggag agcaggactt 1100
ccaggagacc ccgggagtc aggagccaca ggcctgaaag gaagcaaagg 1150
ggacacagga cttcaaggac agcaaggag aaaaggagaa tcaggagtgc 1200
caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcaggt 1250
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aggatcttct ggggagcaag gagtaaagg agaaaaagg gaaagagggt 1350
aaaactcagt gtccgtcagg attgtcgga gtagtaacc aggccgggct 1400
gaagtttact acagtgtac ctgggggaca atttgcatg acgagtggca 1450

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 ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtgca 1650
 gcgtctgacc cggaaacctt ttcacttctc tgctcccag gtgtcctcgg 1700
 gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaac 1750
 tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

Met	Arg	Asn	Lys	Lys	Ile	Leu	Lys	Glu	Asp	Glu	Leu	Leu	Ser	Glu	1	5	10	15
Thr	Gln	Gln	Ala	Ala	Phe	His	Gln	Ile	Ala	Met	Glu	Pro	Phe	Glu	20	25	30	
Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				

185					190					195				
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln
				200					205					210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln
				215					220					225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys
				230					235					240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro
				245					250					255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met
				260					265					270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro
				275					280					285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln
				290					295					300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val
				305					310					315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro
				320					325					330
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr
				335					340					345
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln
				350					355					360
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys
				365					370					375
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro
				380					385					390
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser
				395					400					405
Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn
				410					415					420
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala
				425					430					435
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu
				440					445					450
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr
				455					460					465
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln

470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu		
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His		
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val		
515	520	

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
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 aaaagccaaa atgaaactga tgggtacttgt tttcaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250
 aagatactaa aagatcacia ctgtcacaac cttccggaag gagtagctga 300
 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgccca 400
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
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 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 98
 <212> PRT
 <213> Homo Sapien

<400> 616
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
 1 5 10 15
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
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 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100
 accccgccgt ggtggttgga gggcgcgag tagagcagca gcacaggcgc 150
 gggccccggg aggcgggctc tgctcgcgcc gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250
 ctggggcgct ggtgctggcg ggtgggttct ttctcctcgg ctctccttctc 300
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 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
 tttcagcttg caaagcaaatt tcaatcccag tggaaagaat ttggcctgga 500
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550
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 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700
 atctagtgtg tgtaactat gcacgaactg aagacttctt taaattggaa 750
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800
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 aaggagtcac tctctactcc gaccctgctg actactttgc tcctgggggtg 900
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agtggagcag ctgttggttca tgaaattgtg aggagctttg gaacactgaa 1400
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caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450
 gaatccgtat tgaatttggtg tggtatgtca ctcagaaaga atcgtaatgg 2500
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 atatataa 2558

<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618
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 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
 20 25 30
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90
 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
 95 100 105
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
 110 115 120
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
 125 130 135
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
 140 145 150
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
 155 160 165
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
 170 175 180
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
 185 190 195
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
 200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn Asp	Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50